

SEQUENCE LISTING

<110> NG, Mary Mah Lee
CHU, Justin Jang Hann

<120> Molecules, Compositions, Methods and Kits For Applications
Associated With Flaviviruses

<130> 59419-010100

<140> to be assigned

<141> 2004-01-22

<150> US 60/442,157

<151> 2003-01-22

<160> 19

<170> PatentIn version 3.2

<210> 1

<211> 14

<212> PRT

<213> Vero cells

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<223> Xaa can be any naturally occurring amino acid

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<223> Sequence coding for integrin alpha V subunit

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ccg ctt ctt ctc tcg gga ctc ctg cta cct ctg tgc cgc gcc ttc aac 96
Pro Leu Leu Leu Ser Gly Leu Leu Leu Pro Leu Cys Arg Ala Phe Asn
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cta gac gtg gac agt cct gcc gag tac tct ggc ccc gag gga agt tac 144
Leu Asp Val Asp Ser Pro Ala Glu Tyr Ser Gly Pro Glu Gly Ser Tyr
35 40 45

ttc ggc ttc gcc gtg gat ttc ttc gtg ccc agc gcg tct tcc cgg atg 192
Phe Gly Phe Ala Val Asp Phe Phe Val Pro Ser Ala Ser Ser Arg Met
50 55 60

ttt ctt ctc gtg gga gct ccc aaa gca aac acc acc cag cct ggg att 240
Phe Leu Leu Val Gly Ala Pro Lys Ala Asn Thr Thr Gln Pro Gly Ile
65 70 75 80

gtg gaa gga ggg cag gtc ctc aaa tgt gac tgg tct tct acc cgc cgg 288
Val Glu Gly Gly Gln Val Leu Lys Cys Asp Trp Ser Ser Thr Arg Arg
85 90 95

tgc cag cca att gaa ttt gat gca aca ggc aat aga gat tat gcc aag 336
Cys Gln Pro Ile Glu Phe Asp Ala Thr Gly Asn Arg Asp Tyr Ala Lys
100 105 110

gat gat cca ttg gaa ttt aag tcc cat cag tgg ttt gga gca tct gtg 384
Asp Asp Pro Leu Glu Phe Lys Ser His Gln Trp Phe Gly Ala Ser Val
115 120 125

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Arg Ser Lys Gln Asp Lys Ile Leu Ala Cys Ala Pro Leu Tyr His Trp
130 135 140

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Arg Thr Glu Met Lys Gln Glu Arg Glu Pro Val Gly Thr Cys Phe Leu

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	165	170	175	
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Ile Asp Ala Asp Gly Gln Gly Phe Cys Gln Gly Gly Phe Ser Ile Asp				
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Phe Thr Lys Ala Asp Arg Val Leu Leu Gly Gly Pro Gly Ser Phe Tyr				
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Trp Gln Gly Gln Leu Ile Ser Asp Gln Val Ala Glu Ile Val Ser Lys				
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Tyr Asp Pro Asn Val Tyr Ser Ile Lys Tyr Asn Asn Gln Leu Ala Thr				
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Arg Thr Ala Gln Ala Ile Phe Asp Asp Ser Tyr Leu Gly Tyr Ser Val				
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Ala Val Gly Asp Phe Asn Gly Asp Gly Ile Asp Asp Phe Val Ser Gly				
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Val Pro Arg Ala Ala Arg Thr Leu Gly Met Val Tyr Ile Tyr Asp Gly				
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Lys Asn Met Ser Ser Leu Tyr Asn Phe Thr Gly Glu Gln Met Ala Ala				
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Ala Asp Val Phe Ile Gly Ala Pro Leu Phe Met Asp Arg Gly Ser Asp				
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Gly Lys Leu Gln Glu Val Gly Gln Val Ser Val Ser Leu Gln Arg Ala				
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Arg Phe Gly Ser Ala Ile Ala Pro Leu Gly Asp Leu Asp Gln Asp Gly				
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cca tct caa atc ctt gaa ggg cag tgg gct gct cga agc atg cca cca	1296
Pro Ser Gln Ile Leu Glu Gly Gln Trp Ala Ala Arg Ser Met Pro Pro	
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Ser Phe Gly Tyr Ser Met Lys Gly Ala Thr Asp Ile Asp Lys Asn Gly	
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Tyr Pro Asp Leu Ile Val Gly Ala Phe Gly Val Asp Arg Ala Ile Leu	
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Tyr Arg Ala Arg Pro Val Ile Thr Val Asn Ala Gly Leu Glu Val Tyr	
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Pro Ser Ile Leu Asn Gln Asp Asn Lys Thr Cys Ser Leu Pro Gly Thr	
485 490 495	
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Gly Lys Gly Val Leu Pro Arg Lys Leu Asn Phe Gln Val Glu Leu Leu	
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665

670

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Thr Arg Gly Val Ser Ser Cys Gln Gln Cys Leu Ala Val Ser Pro Met	
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Asp Lys Gly Ser Gly Asp Ser Ser Gln Val Thr Gln Val Ser Pro Gln	
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Arg Ile Ala Leu Arg Leu Arg Pro Asp Asp Ser Lys Asn Phe Ser Ile	
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Gln Val Arg Gln Val Glu Asp Tyr Pro Val Asp Ile Tyr Tyr Leu Met	
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Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Trp Ser Ile Gln Asn Leu	
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165 170 175	
att ggc ttc ggg gca ttt gtg gac aag cct gtg tca cca tac atg tat	576
Ile Gly Phe Gly Ala Phe Val Asp Lys Pro Val Ser Pro Tyr Met Tyr	
180 185 190	
atc tcc cca cca gag gcc ctg gaa aac ccc tgc tat gat atg aag acc	624
Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp Met Lys Thr	
195 200 205	
acc tgc ttg ccc atg ttt ggc tac aaa cac gtg ctg acg cta act gac	672
Thr Cys Leu Pro Met Phe Gly Tyr Lys His Val Leu Thr Leu Thr Asp	
210 215 220	
cag gtg acc cgc ttc aat gag gaa gtg aag aag cag agt gtg tca cgg	720
Gln Val Thr Arg Phe Asn Glu Glu Val Lys Lys Gln Ser Val Ser Arg	
225 230 235 240	

aac cga gat gcc cca gag ggt ggc ttt gat gcc atc atg cag gct aca Asn Arg Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr 245 250 255	768
gtc tgt gat gaa aag att ggc tgg agg aat gat gca tcc cac ttg ctg Val Cys Asp Glu Lys Ile Gly Trp Arg Asn Asp Ala Ser His Leu Leu 260 265 270	816
gtg ttt acc act gat gcc aag act cat ata gca ttg gac gga agg ctg Val Phe Thr Thr Asp Ala Lys Thr His Ile Ala Leu Asp Gly Arg Leu 275 280 285	864
gca ggc att gtc cag cct aat gac ggg cag tgt cat gtt ggt agt gac Ala Gly Ile Val Gln Pro Asn Asp Gly Gln Cys His Val Gly Ser Asp 290 295 300	912
aat cat tac tct gcc tcc act acc atg gat tat ccc tct ttg ggg ctg Asn His Tyr Ser Ala Ser Thr Thr Met Asp Tyr Pro Ser Leu Gly Leu 305 310 315 320	960
atg act gag aag cta tcc cag aaa aac atc aat ttg atc ttt gca gtg Met Thr Glu Lys Leu Ser Gln Lys Asn Ile Asn Leu Ile Phe Ala Val 325 330 335	1008
act gaa aat gta gtc aat ctc tat cag aac tat agt gag ctc atc cca Thr Glu Asn Val Val Asn Leu Tyr Gln Asn Tyr Ser Glu Leu Ile Pro 340 345 350	1056
ggg acc aca gtt ggg gtt ctg tcc atg gat tcc agc aat gtc ctc cag Gly Thr Thr Val Gly Val Leu Ser Met Asp Ser Ser Asn Val Leu Gln 355 360 365	1104
ctc att gtt gat gct tat ggg aaa atc cgt tct aaa gta gag ctg gaa Leu Ile Val Asp Ala Tyr Gly Lys Ile Arg Ser Lys Val Glu Leu Glu 370 375 380	1152
gtg cgt gac ctc cct gaa gag ttg tct cta tcc ttc aat gcc acc tgc Val Arg Asp Leu Pro Glu Glu Leu Ser Leu Ser Phe Asn Ala Thr Cys 385 390 395 400	1200
ctc aac aat gag gtc atc cct ggc ctc aag tct tgt atg gga ctc aag Leu Asn Asn Glu Val Ile Pro Gly Leu Lys Ser Cys Met Gly Leu Lys 405 410 415	1248
att gga gac acg gtg agc ttc agc att gag gcc aag gtg cga ggc tgt Ile Gly Asp Thr Val Ser Phe Ser Ile Glu Ala Lys Val Arg Gly Cys 420 425 430	1296
ccc cag gag aag gag aag tcc ttt acc ata aag ccc gtg ggc ttc aag Pro Gln Glu Lys Glu Lys Ser Phe Thr Ile Lys Pro Val Gly Phe Lys 435 440 445	1344
gac agc ctg atc gtc cag gtc acc ttt gat tgt gac tgt gcc tgc cag Asp Ser Leu Ile Val Gln Val Thr Phe Asp Cys Asp Cys Ala Cys Gln 450 455 460	1392
gcc caa gct gaa cct aat agc cat cgc tgc aac aat ggc aat ggg acc	1440

Ala Gln Ala Glu Pro Asn Ser His Arg Cys Asn Asn Gly Asn Gly Thr	
465 470 475 480	
ttt gag tgt ggg gta tgc cgt tgt ggg cct ggc tgg ctg gga tcc cag	1488
Phe Glu Cys Gly Val Cys Arg Cys Gly Pro Gly Trp Leu Gly Ser Gln	
485 490 495	
tgt gag tgc tca gag gag gac tat cgc cct tcc cag cag gac gaa tgc	1536
Cys Glu Cys Ser Glu Glu Asp Tyr Arg Pro Ser Gln Gln Asp Glu Cys	
500 505 510	
agc ccc cgg gag ggt cag ccc gtc tgc agc cag cgg ggc gag tgc ctc	1584
Ser Pro Arg Glu Gly Gln Pro Val Cys Ser Gln Arg Gly Glu Cys Leu	
515 520 525	
tgt ggt caa tgt gtc tgc cac agc agt gac ttt ggc aag atc acg ggc	1632
Cys Gly Gln Cys Val Cys His Ser Ser Asp Phe Gly Lys Ile Thr Gly	
530 535 540	
aag tac tgc gag tgt gac gac ttc tcc tgt gtc cgc tac aag ggg gag	1680
Lys Tyr Cys Glu Cys Asp Asp Phe Ser Cys Val Arg Tyr Lys Gly Glu	
545 550 555 560	
atg tgc tca ggc cat ggc cag tgc agc tgt ggg gac tgc ctg tgt gac	1728
Met Cys Ser Gly His Gly Gln Cys Ser Cys Gly Asp Cys Leu Cys Asp	
565 570 575	
tcc gac tgg acc ggc tac tac tgc aac tgt acc acg cgt act gac acc	1776
Ser Asp Trp Thr Gly Tyr Tyr Cys Asn Cys Thr Thr Arg Thr Asp Thr	
580 585 590	
tgc atg tcc agc aat ggg ctg ctg tgc agc ggc cgc ggc aag tgt gaa	1824
Cys Met Ser Ser Asn Gly Leu Cys Ser Gly Arg Gly Lys Cys Glu	
595 600 605	
tgt ggc agc tgt gtc tgt atc cag ccg ggc tcc tat ggg gac acc tgt	1872
Cys Gly Ser Cys Val Cys Ile Gln Pro Gly Ser Tyr Gly Asp Thr Cys	
610 615 620	
gag aag tgc ccc acc tgc cca gat gcc tgc acc ttt aag aaa gaa tgt	1920
Glu Lys Cys Pro Thr Cys Pro Asp Ala Cys Thr Phe Lys Lys Glu Cys	
625 630 635 640	
gtg gag tgt aag aag ttt gac cgg gag ccc tac atg acc gaa aat acc	1968
Val Glu Cys Lys Lys Phe Asp Arg Glu Pro Tyr Met Thr Glu Asn Thr	
645 650 655	
tgc aac cgt tac tgc cgt gac gag att gag tca gtg aaa gag ctt aag	2016
Cys Asn Arg Tyr Cys Arg Asp Glu Ile Glu Ser Val Lys Glu Leu Lys	
660 665 670	
gac act ggc aag gat gca gtg aat tgt acc tat aag aat gag gat gac	2064
Asp Thr Gly Lys Asp Ala Val Asn Cys Thr Tyr Lys Asn Glu Asp Asp	
675 680 685	
tgt gtc gtc aga ttc cag tac tat gaa gat tct agt gga aag tcc atc	2112
Cys Val Val Arg Phe Gln Tyr Tyr Glu Asp Ser Ser Gly Lys Ser Ile	

690	695	700	
ctg tat gtg gta gaa gag cca gag tgt ccc aag ggc cct gac atc ctg			2160
Leu Tyr Val Val Glu Glu Pro Glu Cys Pro Lys Gly Pro Asp Ile Leu			
705	710	715	720
gtg gtc ctg ctc tca gtg atg ggg gcc att ctg ctc att ggc ctt gcc			2208
Val Val Leu Leu Ser Val Met Gly Ala Ile Leu Leu Ile Gly Leu Ala			
	725	730	735
gcc ctg ctc atc tgg aaa ctc ctc atc acc atc cac gac cga aaa gaa			2256
Ala Leu Leu Ile Trp Lys Leu Leu Ile Thr Ile His Asp Arg Lys Glu			
	740	745	750
ttc gct aaa ttt gag gaa gaa cgc gcc aga gca aaa tgg gac aca gcc			2304
Phe Ala Lys Phe Glu Glu Glu Arg Ala Arg Ala Lys Trp Asp Thr Ala			
	755	760	765
aac aac cca ctg tat aaa gag gcc acg tct acc ttc acc aat atc acg			2352
Asn Asn Pro Leu Tyr Lys Glu Ala Thr Ser Thr Phe Thr Asn Ile Thr			
	770	775	780
tac cgg ggc act taa			2367
Tyr Arg Gly Thr			
785			

<210> 11
 <211> 788
 <212> PRT
 <213> Homo Sapiens

<400> 11

Met Arg Ala Arg Pro Arg Pro Arg Pro Leu Trp Ala Thr Val Leu Ala			
1	5	10	15
Leu Gly Ala Leu Ala Gly Val Gly Val Gly Gly Pro Asn Ile Cys Thr			
	20	25	30
Thr Arg Gly Val Ser Ser Cys Gln Gln Cys Leu Ala Val Ser Pro Met			
	35	40	45
Cys Ala Trp Cys Ser Asp Glu Ala Leu Pro Leu Gly Ser Pro Arg Cys			
	50	55	60
Asp Leu Lys Glu Asn Leu Leu Lys Asp Asn Cys Ala Pro Glu Ser Ile			
	65	70	75
			80
Glu Phe Pro Val Ser Glu Ala Arg Val Leu Glu Asp Arg Pro Leu Ser			
	85	90	95

Asp Lys Gly Ser Gly Asp Ser Ser Gln Val Thr Gln Val Ser Pro Gln
100 105 110

Arg Ile Ala Leu Arg Leu Arg Pro Asp Asp Ser Lys Asn Phe Ser Ile
115 120 125

Gln Val Arg Gln Val Glu Asp Tyr Pro Val Asp Ile Tyr Tyr Leu Met
130 135 140

Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Trp Ser Ile Gln Asn Leu
145 150 155 160

Gly Thr Lys Leu Ala Thr Gln Met Arg Lys Leu Thr Ser Asn Leu Arg
165 170 175

Ile Gly Phe Gly Ala Phe Val Asp Lys Pro Val Ser Pro Tyr Met Tyr
180 185 190

Ile Ser Pro Pro Glu Ala Leu Glu Asn Pro Cys Tyr Asp Met Lys Thr
195 200 205

Thr Cys Leu Pro Met Phe Gly Tyr Lys His Val Leu Thr Leu Thr Asp
210 215 220

Gln Val Thr Arg Phe Asn Glu Glu Val Lys Lys Gln Ser Val Ser Arg
225 230 235 240

Asn Arg Asp Ala Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Ala Thr
245 250 255

Val Cys Asp Glu Lys Ile Gly Trp Arg Asn Asp Ala Ser His Leu Leu
260 265 270

Val Phe Thr Thr Asp Ala Lys Thr His Ile Ala Leu Asp Gly Arg Leu
275 280 285

Ala Gly Ile Val Gln Pro Asn Asp Gly Gln Cys His Val Gly Ser Asp
290 295 300

Asn His Tyr Ser Ala Ser Thr Thr Met Asp Tyr Pro Ser Leu Gly Leu
305 310 315 320

Met Thr Glu Lys Leu Ser Gln Lys Asn Ile Asn Leu Ile Phe Ala Val
325 330 335

Thr Glu Asn Val Val Asn Leu Tyr Gln Asn Tyr Ser Glu Leu Ile Pro
340 345 350

Gly Thr Thr Val Gly Val Leu Ser Met Asp Ser Ser Asn Val Leu Gln
355 360 365

Leu Ile Val Asp Ala Tyr Gly Lys Ile Arg Ser Lys Val Glu Leu Glu
370 375 380

Val Arg Asp Leu Pro Glu Glu Leu Ser Leu Ser Phe Asn Ala Thr Cys
385 390 395 400

Leu Asn Asn Glu Val Ile Pro Gly Leu Lys Ser Cys Met Gly Leu Lys
405 410 415

Ile Gly Asp Thr Val Ser Phe Ser Ile Glu Ala Lys Val Arg Gly Cys
420 425 430

Pro Gln Glu Lys Glu Lys Ser Phe Thr Ile Lys Pro Val Gly Phe Lys
435 440 445

Asp Ser Leu Ile Val Gln Val Thr Phe Asp Cys Asp Cys Ala Cys Gln
450 455 460

Ala Gln Ala Glu Pro Asn Ser His Arg Cys Asn Asn Gly Asn Gly Thr
465 470 475 480

Phe Glu Cys Gly Val Cys Arg Cys Gly Pro Gly Trp Leu Gly Ser Gln
485 490 495

Cys Glu Cys Ser Glu Glu Asp Tyr Arg Pro Ser Gln Gln Asp Glu Cys
500 505 510

Ser Pro Arg Glu Gly Gln Pro Val Cys Ser Gln Arg Gly Glu Cys Leu
515 520 525

Cys Gly Gln Cys Val Cys His Ser Ser Asp Phe Gly Lys Ile Thr Gly
530 535 540

Lys Tyr Cys Glu Cys Asp Asp Phe Ser Cys Val Arg Tyr Lys Gly Glu

545	550	555	560
Met Cys Ser Gly His Gly Gln Cys Ser Cys Gly Asp Cys Leu Cys Asp			
	565	570	575
Ser Asp Trp Thr Gly Tyr Tyr Cys Asn Cys Thr Thr Arg Thr Asp Thr			
	580	585	590
Cys Met Ser Ser Asn Gly Leu Leu Cys Ser Gly Arg Gly Lys Cys Glu			
	595	600	605
Cys Gly Ser Cys Val Cys Ile Gln Pro Gly Ser Tyr Gly Asp Thr Cys			
	610	615	620
Glu Lys Cys Pro Thr Cys Pro Asp Ala Cys Thr Phe Lys Lys Glu Cys			
	625	630	635
Val Glu Cys Lys Lys Phe Asp Arg Glu Pro Tyr Met Thr Glu Asn Thr			
	645	650	655
Cys Asn Arg Tyr Cys Arg Asp Glu Ile Glu Ser Val Lys Glu Leu Lys			
	660	665	670
Asp Thr Gly Lys Asp Ala Val Asn Cys Thr Tyr Lys Asn Glu Asp Asp			
	675	680	685
Cys Val Val Arg Phe Gln Tyr Tyr Glu Asp Ser Ser Gly Lys Ser Ile			
	690	695	700
Leu Tyr Val Val Glu Glu Pro Glu Cys Pro Lys Gly Pro Asp Ile Leu			
	705	710	715
Val Val Leu Leu Ser Val Met Gly Ala Ile Leu Leu Ile Gly Leu Ala			
	725	730	735
Ala Leu Leu Ile Trp Lys Leu Leu Ile Thr Ile His Asp Arg Lys Glu			
	740	745	750
Phe Ala Lys Phe Glu Glu Glu Arg Ala Arg Ala Lys Trp Asp Thr Ala			
	755	760	765
Asn Asn Pro Leu Tyr Lys Glu Ala Thr Ser Thr Phe Thr Asn Ile Thr			
	770	775	780

Tyr Arg Gly Thr
785

<210> 12
<211> 64
<212> DNA
<213> Synthetic DNA

<220>
<221> misc_feature
<222> (1)..(64)
<223> Integrin sequence alpha V1

<400> 12
gatcccgga ttgtttatat cttcattcaa gagatgaaga tataaacaat tccttttttg 60
gaaa 64

<210> 13
<211> 64
<212> DNA
<213> Synthetic DNA

<220>
<221> misc_feature
<222> (1)..(64)
<223> Integrin sequence alpha V2

<400> 13
gatcccgact ttctgtgca ttttaattcaa gagattaaat gcacaggaaa gtcttttttg 60
gaaa 64

<210> 14
<211> 63
<212> DNA
<213> Synthetic DNA

<220>
<221> misc_feature
<222> (1)..(63)
<223> Integrin sequence beta 31

<400> 14
gatcccacat caatttgatc ttgtcttcaa gagagcaaag atcaaattga tggttttttg 60
aaa 63

<210> 15
 <211> 64
 <212> DNA
 <213> Synthetic DNA

<220>
 <221> misc_feature
 <222> (1)..(64)
 <223> Integrin sequence beta 32

<400> 15
 gatccgttgt acctataaga atgagttcaa gagactcatt cttataggta caattttttg 60
 gaaa 64

<210> 16
 <211> 1233
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1233)
 <223> Sequence coding for neurotensin receptor

<400> 16
 atg gaa acc agc agc ccg cgg ccc ccg cgg ccc agc tcc aac ccg ggg 48
 Met Glu Thr Ser Ser Pro Arg Pro Pro Arg Pro Ser Ser Asn Pro Gly
 1 5 10 15
 ctg agc ctg gac gcc cgg ctg ggc gtg gac act cgc ctc tgg gcc aag 96
 Leu Ser Leu Asp Ala Arg Leu Gly Val Asp Thr Arg Leu Trp Ala Lys
 20 25 30
 gtg ctg ttc acc gcg ctc tac gca ctc atc tgg gcg ctg ggc gcg gcg 144
 Val Leu Phe Thr Ala Leu Tyr Ala Leu Ile Trp Ala Leu Gly Ala Ala
 35 40 45
 ggc aat gcg ctg tcc gtg cac gtg gtg ctg aag gcg cgg gcc ggg cgc 192
 Gly Asn Ala Leu Ser Val His Val Val Leu Lys Ala Arg Ala Gly Arg
 50 55 60
 gcg ggg cgc ctg cgc cac cac gtg ctc agc ctg gcg ctc gcg ggc ctg 240
 Ala Gly Arg Leu Arg His His Val Leu Ser Leu Ala Leu Ala Gly Leu
 65 70 75 80
 ctg ctg ctg ctg gtc ggc gtg ccg gtg gag ctc tac agc ttc gtg tgg 288
 Leu Leu Leu Leu Val Gly Val Pro Val Glu Leu Tyr Ser Phe Val Trp
 85 90 95
 ttc cac tac ccc tgg gtc ttc ggc gac ctg ggc tgc cgc ggc tac tac 336
 Phe His Tyr Pro Trp Val Phe Gly Asp Leu Gly Cys Arg Gly Tyr Tyr
 100 105 110

ttc gtg cac gag ctg tgc gcc tac gcc acg gtg ctg agc gtg gca ggc	384
Phe Val His Glu Leu Cys Ala Tyr Ala Thr Val Leu Ser Val Ala Gly	
115 120 125	
ctg agc gcc gag cgc tgc cta gcc gtg tgc cag ccc ctg cgt gcc cgc	432
Leu Ser Ala Glu Arg Cys Leu Ala Val Cys Gln Pro Leu Arg Ala Arg	
130 135 140	
agc ctg ctg acg cca cgc cgg acc cgg tgg ctg gtg gcg ctc tcg tgg	480
Ser Leu Leu Thr Pro Arg Arg Thr Arg Trp Leu Val Ala Leu Ser Trp	
145 150 155 160	
gcc gcc tcg ctc ggc ctc gcc ctg ccc atg gcc gtc atc atg ggg cag	528
Ala Ala Ser Leu Gly Leu Ala Leu Pro Met Ala Val Ile Met Gly Gln	
165 170 175	
aag cac gaa ctc gag acg gcg gac ggg gag ccg gag ccc gcc tcg cga	576
Lys His Glu Leu Glu Thr Ala Asp Gly Glu Pro Glu Pro Ala Ser Arg	
180 185 190	
gtg tgc acg gtg ctg gtg agc cgc acc gcg ctc caa gtc ttt atc cag	624
Val Cys Thr Val Leu Val Ser Arg Thr Ala Leu Gln Val Phe Ile Gln	
195 200 205	
gtg aat gtg ctg gtg tcc ttc gtg ctc ccc ttg gca cta act gct ttc	672
Val Asn Val Leu Val Ser Phe Val Leu Pro Leu Ala Leu Thr Ala Phe	
210 215 220	
ctg aat ggg gtc aca gtg agc cac ctg ctg gcc ctc tgc tcc caa gtg	720
Leu Asn Gly Val Thr Val Ser His Leu Leu Ala Leu Cys Ser Gln Val	
225 230 235 240	
ccg tcc act tct acc ccg ggc agc tcc acc ccc agc cgc ctg gag ctg	768
Pro Ser Thr Ser Thr Pro Gly Ser Ser Thr Pro Ser Arg Leu Glu Leu	
245 250 255	
ctg agt gag gag ggt ctc ctc agc ttc atc gta tgg aag aag acc ttt	816
Leu Ser Glu Glu Gly Leu Leu Ser Phe Ile Val Trp Lys Lys Thr Phe	
260 265 270	
atc cag gga ggc cag gtc agc ctg gtg aga cat aaa gac gtg cgc cgg	864
Ile Gln Gly Gly Gln Val Ser Leu Val Arg His Lys Asp Val Arg Arg	
275 280 285	
atc cgc agc ctc cag cgc agc gtc cag gtt ctc aga gcc atc gtg gtc	912
Ile Arg Ser Leu Gln Arg Ser Val Gln Val Leu Arg Ala Ile Val Val	
290 295 300	
atg tat gtc atc tgc tgg ctg ccg tac cat gcc cgc agg ctc atg tac	960
Met Tyr Val Ile Cys Trp Leu Pro Tyr His Ala Arg Arg Leu Met Tyr	
305 310 315 320	
tgc tac gta cct gat gac gcg tgg act gac cca ctg tac aat ttc tac	1008
Cys Tyr Val Pro Asp Asp Ala Trp Thr Asp Pro Leu Tyr Asn Phe Tyr	
325 330 335	
cac tac ttc tac atg gtg acc aac aca ctt ttc tac gtc agc tca gct	1056

His Tyr Phe Tyr Met Val Thr Asn Thr Leu Phe Tyr Val Ser Ser Ala
 340 345 350

gtg act cct ctt ctc tac aac gcc gtg tcc tcc tcc ttc aga aaa ctc 1104
 Val Thr Pro Leu Leu Tyr Asn Ala Val Ser Ser Ser Phe Arg Lys Leu
 355 360 365

ttc ctg gaa gcc gtc agc tcc ctg tgt gga gag cac cac ccc atg aag 1152
 Phe Leu Glu Ala Val Ser Ser Leu Cys Gly Glu His His Pro Met Lys
 370 375 380

cgg tta ccc ccg aag ccc cag agt ccc acc cta atg gat aca gct tca 1200
 Arg Leu Pro Pro Lys Pro Gln Ser Pro Thr Leu Met Asp Thr Ala Ser
 385 390 395 400

ggc ttt ggg gat ccc cca gaa acc cgg acc tga 1233
 Gly Phe Gly Asp Pro Pro Glu Thr Arg Thr
 405 410

<210> 17
 <211> 410
 <212> PRT
 <213> Homo sapiens

<400> 17

Met Glu Thr Ser Ser Pro Arg Pro Pro Arg Pro Ser Ser Asn Pro Gly
 1 5 10 15

Leu Ser Leu Asp Ala Arg Leu Gly Val Asp Thr Arg Leu Trp Ala Lys
 20 25 30

Val Leu Phe Thr Ala Leu Tyr Ala Leu Ile Trp Ala Leu Gly Ala Ala
 35 40 45

Gly Asn Ala Leu Ser Val His Val Val Leu Lys Ala Arg Ala Gly Arg
 50 55 60

Ala Gly Arg Leu Arg His His Val Leu Ser Leu Ala Leu Ala Gly Leu
 65 70 75 80

Leu Leu Leu Leu Val Gly Val Pro Val Glu Leu Tyr Ser Phe Val Trp
 85 90 95

Phe His Tyr Pro Trp Val Phe Gly Asp Leu Gly Cys Arg Gly Tyr Tyr
 100 105 110

Phe Val His Glu Leu Cys Ala Tyr Ala Thr Val Leu Ser Val Ala Gly
 115 120 125

Leu Ser Ala Glu Arg Cys Leu Ala Val Cys Gln Pro Leu Arg Ala Arg
130 135 140

Ser Leu Leu Thr Pro Arg Arg Thr Arg Trp Leu Val Ala Leu Ser Trp
145 150 155 160

Ala Ala Ser Leu Gly Leu Ala Leu Pro Met Ala Val Ile Met Gly Gln
165 170 175

Lys His Glu Leu Glu Thr Ala Asp Gly Glu Pro Glu Pro Ala Ser Arg
180 185 190

Val Cys Thr Val Leu Val Ser Arg Thr Ala Leu Gln Val Phe Ile Gln
195 200 205

Val Asn Val Leu Val Ser Phe Val Leu Pro Leu Ala Leu Thr Ala Phe
210 215 220

Leu Asn Gly Val Thr Val Ser His Leu Leu Ala Leu Cys Ser Gln Val
225 230 235 240

Pro Ser Thr Ser Thr Pro Gly Ser Ser Thr Pro Ser Arg Leu Glu Leu
245 250 255

Leu Ser Glu Glu Gly Leu Leu Ser Phe Ile Val Trp Lys Lys Thr Phe
260 265 270

Ile Gln Gly Gly Gln Val Ser Leu Val Arg His Lys Asp Val Arg Arg
275 280 285

Ile Arg Ser Leu Gln Arg Ser Val Gln Val Leu Arg Ala Ile Val Val
290 295 300

Met Tyr Val Ile Cys Trp Leu Pro Tyr His Ala Arg Arg Leu Met Tyr
305 310 315 320

Cys Tyr Val Pro Asp Asp Ala Trp Thr Asp Pro Leu Tyr Asn Phe Tyr
325 330 335

His Tyr Phe Tyr Met Val Thr Asn Thr Leu Phe Tyr Val Ser Ser Ala
340 345 350

Val Thr Pro Leu Leu Tyr Asn Ala Val Ser Ser Ser Phe Arg Lys Leu
355 360 365

Phe Leu Glu Ala Val Ser Ser Leu Cys Gly Glu His His Pro Met Lys
370 375 380

Arg Leu Pro Pro Lys Pro Gln Ser Pro Thr Leu Met Asp Thr Ala Ser
385 390 395 400

Gly Phe Gly Asp Pro Pro Glu Thr Arg Thr
405 410

<210> 18
<211> 65
<212> DNA
<213> Synthetic DNA

<220>
<221> misc_feature
<222> (1)..(65)
<223> Functional sequence of neurotensin receptor used for siRNA

<400> 18
gatcccggtta tgacttttgg acagtcttca agagagactg tccaaaagtc ataatttttt 60
ggaaa 65

<210> 19
<211> 14
<212> PRT
<213> West Nile Virus

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa can be any naturally occurring amino acid

<400> 19

Ser Ile Pro Lys Leu Glu Ile Ala Gly Xaa Phe Lys Asp Leu
1 5 10